

N. Nimmig

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Page 1 of 7

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Harry  
July 28, 01

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/298,523C

DATE: 06/01/2001

TIME: 14:07:44

Input Set : A:\00011770.app

Output Set : C:\CRF3\06012001\I298523C.raw

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NOV 08 2002

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3 <110> APPLICANT: BRILES et al.  
5 <120> TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS  
6 AND STRAINS THEREOF AND USES THEREFOR  
8 <130> FILE REFERENCE: 454312-3140  
10 <140> CURRENT APPLICATION NUMBER: 09/298,523C  
11 <141> CURRENT FILING DATE: 1999-04-23  
13 <160> NUMBER OF SEQ ID NOS: 78  
15 <170> SOFTWARE: PatentIn Ver. 2.1  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 691  
19 <212> TYPE: PRT  
20 <213> ORGANISM: Streptococcus pneumoniae  
22 <400> SEQUENCE: 1  
23 Met Phe Ala Ser Lys Ser Glu Arg Lys Val His Tyr Ser Ile Arg Lys  
24 1 5 10 15  
26 Phe Ser Ile Gly Val Ala Ser Val Ala Val Ala Ser Leu Phe Leu Gly  
27 20 25 30  
29 Gly Val Val His Ala Glu Gly Val Arg Ser Gly Asn Asn Leu Thr Val  
30 35 40 45  
32 Thr Ser Ser Gly Gln Asp Ile Ser Lys Lys Tyr Ala Asp Glu Val Glu  
33 50 55 60  
35 Ser His Leu Glu Ser Ile Leu Lys Asp Val Lys Lys Asn Leu Lys Lys  
36 65 70 75 80  
38 Val Gln His Thr Gln Asn Val Gly Leu Ile Thr Lys Leu Ser Glu Ile  
39 85 90 95  
41 Lys Lys Lys Tyr Leu Tyr Asp Leu Lys Val Asn Val Leu Ser Glu Ala  
42 100 105 110  
44 Glu Leu Thr Ser Lys Thr Lys Glu Thr Lys Glu Lys Leu Thr Ala Thr  
45 115 120 125  
47 Phe Glu Gln Phe Lys Lys Asp Thr Leu Pro Thr Glu Pro Glu Lys Lys  
48 130 135 140  
50 Val Ala Glu Ala Gln Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu  
51 145 150 155 160  
53 Asp Gln Lys Glu Lys Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys  
54 165 170 175  
56 Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala  
57 180 185 190  
59 Glu Leu Glu Leu Val Lys Val Lys Ala Lys Glu Ser Gln Asp Glu Glu  
60 195 200 205  
62 Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln Ala Glu Ala  
63 210 215 220  
65 Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala Lys Arg Lys  
66 225 230 235 240  
68 Ala Asp Ala Lys Leu Lys Glu Ala Val Glu Lys Asn Val Ala Thr Ser  
69 245 250 255  
71 Glu Gln Asp Lys Pro Lys Arg Arg Ala Lys Arg Gly Val Ser Gly Glu  
72 260 265 270

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```

74 Leu Ala Thr Pro Asp Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser
75      275      280      285
77 Ser Val Gly Glu Glu Thr Leu Pro Ser Pro Ser Leu Asn Met Ala Asn
78      290      295      300
80 Glu Ser Gln Thr Glu His Arg Lys Asp Val Asp Glu Tyr Ile Lys Lys
81 305      310      315      320
83 Met Leu Ser Glu Ile Gln Leu Asp Arg Arg Lys His Thr Gln Asn Val
84      325      330      335
86 Asn Leu Asn Ile Lys Leu Ser Ala Ile Lys Thr Lys Tyr Leu Tyr Glu
87      340      345      350
89 Leu Ser Val Leu Lys Glu Asn Ser Lys Lys Glu Glu Leu Thr Ser Lys
90      355      360      365
92 Thr Lys Ala Glu Leu Thr Ala Ala Phe Glu Gln Phe Lys Lys Asp Thr
93      370      375      380
95 Leu Lys Pro Glu Lys Lys Val Ala Glu Ala Glu Lys Lys Val Glu Glu
96 385      390      395      400
98 Ala Lys Lys Lys Ala Lys Asp Gln Lys Glu Glu Asp Arg Arg Asn Tyr
99      405      410      415
101 Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp
102      420      425      430
104 Val Lys Val Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Glu Ala Asn
105      435      440      445
107 Glu Ser Arg Asn Glu Glu Lys Ile Lys Gln Ala Lys Glu Lys Val Glu
108      450      455      460
110 Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu Lys Ile Lys Thr Asp Arg
111 465      470      475      480
113 Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys
114      485      490      495
116 Lys Ala Ala Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Tyr Ala Leu
117      500      505      510
119 Glu Ala Lys Ile Ala Glu Leu Glu Tyr Glu Val Gln Arg Leu Glu Lys
120      515      520      525
122 Glu Leu Lys Glu Ile Asp Glu Ser Asp Ser Glu Asp Tyr Leu Lys Glu
123      530      535      540
125 Gly Leu Arg Ala Pro Leu Gln Ser Lys Leu Asp Thr Lys Lys Ala Lys
126 545      550      555      560
128 Leu Ser Lys Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala
129      565      570      575
131 Glu Ile Ala Lys Leu Glu Val Gln Leu Lys Asp Ala Glu Gly Asn Asn
132      580      585      590
134 Asn Val Glu Ala Tyr Phe Lys Glu Gly Leu Glu Lys Thr Thr Ala Glu
135      595      600      605
137 Lys Lys Ala Glu Leu Glu Lys Ala Glu Ala Asp Leu Lys Lys Ala Val
138      610      615      620
140 Asp Glu Pro Glu Thr Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro
141 625      630      635      640
143 Glu Lys Pro Ala Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro
144      645      650      655
146 Ala Pro Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Pro

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```

147          660          665          670
149 Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Thr Pro Glu Thr
150          675          680          685
152 Pro Lys Thr
153          690
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 707
158 <212> TYPE: PRT
159 <213> ORGANISM: Streptococcus pneumoniae
161 <400> SEQUENCE: 2
162 Met Phe Ala Ser Lys Ser Glu Arg Lys Val His Tyr Ser Ile Arg Lys
163   1          5          10          15
165 Phe Ser Ile Gly Val Ala Ser Val Ala Val Ala Ser Leu Phe Leu Gly
166          20          25          30
168 Gly Val Val His Ala Glu Gly Val Arg Ser Gly Asn Asn Leu Thr Val
169          35          40          45
171 Thr Ser Ser Gly Gln Asp Ile Ser Lys Lys Tyr Ala Asp Glu Val Glu
172          50          55          60
174 Ser His Leu Glu Ser Ile Leu Lys Asp Val Lys Lys Asn Leu Lys Lys
175   65          70          75          80
177 Val Gln His Thr Gln Asn Val Gly Leu Ile Thr Lys Leu Ser Glu Ile
178          85          90          95
180 Lys Lys Lys Tyr Leu Tyr Asp Leu Lys Val Asn Val Leu Ser Glu Ala
181          100          105          110
183 Glu Leu Thr Ser Lys Thr Lys Glu Thr Lys Glu Lys Leu Thr Ala Thr
184          115          120          125
186 Phe Glu Gln Phe Lys Lys Asp Thr Leu Pro Thr Glu Pro Glu Lys Lys
187          130          135          140
189 Val Ala Glu Ala Gln Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu
190  145          150          155          160
192 Asp Gln Lys Glu Lys Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys
193          165          170          175
195 Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala
196          180          185          190
198 Glu Leu Glu Leu Val Lys Val Lys Ala Lys Glu Ser Gln Asp Glu Glu
199          195          200          205
201 Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln Ala Glu Ala
202          210          215          220
204 Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala Lys Arg Lys
205  225          230          235          240
207 Ala Asp Ala Lys Leu Lys Glu Ala Val Glu Lys Asn Val Ala Thr Ser
208          245          250          255
210 Glu Gln Asp Lys Pro Lys Arg Arg Ala Lys Arg Gly Val Ser Gly Glu
211          260          265          270
213 Leu Ala Thr Pro Asp Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser
214          275          280          285
216 Ser Val Gly Glu Glu Thr Leu Pro Ser Pro Ser Leu Asn Met Ala Asn
217          290          295          300
219 Glu Ser Gln Thr Glu His Arg Lys Asp Val Asp Glu Tyr Ile Lys Lys

```

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```

220 305          310          315          320
222 Met Leu Ser Glu Ile Gln Leu Asp Gly Arg Lys His Thr Pro Asn Val
223          325          330          335
225 Asn Leu Asn Ile Lys Leu Ser Ala Ile Lys Thr Lys Tyr Leu Tyr Glu
226          340          345          350
228 Leu Ser Val Leu Lys Glu Asn Ser Lys Lys Glu Glu Leu Thr Ser Lys
229          355          360          365
231 Thr Lys Ala Glu Leu Thr Ala Ala Phe Glu Gln Phe Lys Lys Asp Thr
232          370          375          380
234 Leu Lys Pro Glu Lys Lys Val Ala Glu Ala Glu Lys Lys Val Glu Glu
235 385          390          395          400
237 Ala Lys Lys Lys Ala Lys Asp Gln Lys Glu Glu Asp Arg Arg Asn Tyr
238          405          410          415
240 Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp
241          420          425          430
243 Val Lys Val Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Glu Ala Asn
244          435          440          445
246 Glu Ser Arg Asn Glu Glu Lys Ile Lys Gln Ala Lys Glu Lys Val Glu
247          450          455          460
249 Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu Lys Ile Lys Thr Asp Arg
250 465          470          475          480
252 Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys
253          485          490          495
255 Lys Ala Ala Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Tyr Ala Leu
256          500          505          510
258 Glu Ala Lys Ile Ala Glu Leu Glu Tyr Glu Val Gln Arg Leu Glu Lys
259          515          520          525
261 Glu Leu Lys Glu Ile Asp Glu Ser Asp Ser Glu Asp Tyr Leu Lys Glu
262          530          535          540
264 Gly Leu Arg Ala Pro Leu Gln Ser Lys Leu Asp Thr Lys Lys Ala Lys
265 545          550          555          560
267 Leu Ser Lys Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala
268          565          570          575
270 Glu Ile Ala Lys Leu Glu Val Gln Leu Lys Asp Ala Glu Gly Asn Asn
271          580          585          590
273 Asn Val Glu Ala Tyr Phe Lys Glu Gly Leu Glu Lys Thr Thr Ala Glu
274          595          600          605
276 Lys Lys Ala Glu Leu Glu Lys Ala Glu Ala Asp Leu Lys Lys Ala Val
277          610          615          620
279 Asp Glu Pro Glu Thr Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro
280 625          630          635          640
282 Glu Lys Pro Ala Glu Lys Pro Ala Pro Ala Pro Ala Pro Glu Lys Pro
283          645          650          655
285 Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro
286          660          665          670
288 Ala Pro Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Pro
289          675          680          685
291 Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Thr Pro Lys
292          690          695          700

```

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294 Pro Glu Thr
295 705
298 <210> SEQ ID NO: 3
299 <211> LENGTH: 711
300 <212> TYPE: PRT
301 <213> ORGANISM: Streptococcus pneumoniae
303 <400> SEQUENCE: 3
304 Met Phe Ala Ser Lys Ser Glu Arg Lys Val His Tyr Ser Ile Arg Lys
305 1 5 10 15
307 Phe Ser Ile Gly Val Ala Ser Val Val Val Ala Ser Leu Val Met Gly
308 20 25 30
310 Ser Val Val His Ala Thr Glu Asn Glu Gly Ile Thr Gln Val Ala Thr
311 35 40 45
313 Ser Tyr Asn Lys Ala Asn Glu Ser Gln Thr Glu His Arg Lys Ala Ala
314 50 55 60
316 Lys Gln Val Asp Glu Asp Ile Lys Lys Met Leu Ser Glu Ile Gln Glu
317 65 70 75 80
319 Tyr Ile Lys Lys Met Leu Ser Glu Ile Gln Leu Asp Lys Arg Lys His
320 85 90 95
322 Thr Gln Asn Val Asn Leu Asn Arg Lys Leu Ser Ala Ile Gln Thr Lys
323 100 105 110
325 Tyr Leu Tyr Glu Leu Arg Val Leu Lys Glu Lys Ser Lys Lys Glu Glu
326 115 120 125
328 Leu Thr Ser Lys Thr Lys Lys Glu Leu Asp Ala Ala Phe Glu Lys Phe
329 130 135 140
331 Lys Lys Glu Glu Pro Glu Leu Thr Lys Lys Leu Ala Glu Ala Lys Gln
332 145 150 155 160
334 Lys Ala Lys Ala Gln Lys Glu Glu Asp Phe Arg Asn Tyr Pro Thr Asn
335 165 170 175
337 Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Phe Asp Val Lys Val
338 180 185 190
340 Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Glu Ala Lys Pro Arg Asn
341 195 200 205
343 Glu Glu Lys Ile Lys Gln Ala Lys Ala Lys Val Glu Ser Lys Lys Ala
344 210 215 220
346 Glu Ala Thr Arg Leu Glu Glu Ile Lys Thr Glu Arg Lys Lys Ala Glu
347 225 230 235 240
349 Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys Lys Ala Ala Glu
350 245 250 255
352 Ala Lys Gln Lys Val Asp Thr Lys Glu Gln Gly Lys Pro Lys Arg Arg
353 260 265 270
355 Ala Lys Arg Gly Val Ser Gly Glu Leu Ala Thr Pro Asp Lys Lys Glu
356 275 280 285
358 Asn Asp Ala Lys Ser Ser Asp Ser Ser Val Gly Glu Glu Thr Leu Pro
359 290 295 300
361 Ser Pro Ser Leu Asn Ala Met Ala Asn Glu Ser Gln Thr Glu His Arg
362 305 310 315 320
364 Lys Asp Val Asp Glu Tyr Ile Lys Lys Met Leu Ser Glu Ile Gln Leu
365 325 330 335

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

**VERIFICATION SUMMARY**

DATE: 06/01/2001

PATENT APPLICATION: US/09/298,523C

TIME: 14:07:45

Input Set : A:\00011770.app

Output Set: C:\CRF3\06012001\I298523C.raw

L:1669 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28

L:4354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71

L:4492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74